



4

SEQUENCE LISTING

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Bentzien, Frauke

<120> Novel Antiangiogenic Peptide Agents and Their Therapeutic and Diagnostic Use

<130> UCSF-018/02US

<140> 09/819,094

<141> 2001-03-27

<150> 09/076,675

<151> 1998-05-12

<150> 60/046,394

<151> 1997-05-12

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Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
115 120 125

Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu
130 135 140

Asn Glu Ile Tyr Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala
145 150 155 160

Asp Glu Glu Ser Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu
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<212> PRT

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| Leu | Ser | Ser | Glu | Met | Phe | Ser | Glu | Phe | Asp | Lys | Arg | Tyr | Thr | His | Gly |
| 35 | | | | | | | 40 | | | | | | 45 | | |
| Arg | Gly | Phe | Ile | Thr | Lys | Ala | Ile | Asn | Ser | Ser | His | Thr | Ser | Ser | Leu |
| 50 | | | | | | | 55 | | | | | 60 | | | |
| Ala | Thr | Pro | Glu | Asp | Lys | Glu | Gln | Ala | Gln | Gln | Met | Asn | Gln | Lys | Asp |
| 65 | | | | | | | 70 | | | | 75 | | 80 | | |
| Phe | Leu | Ser | Leu | Ile | Val | Ser | Ile | Leu | Arg | Ser | Trp | Asn | Glu | Pro | Leu |
| 85 | | | | | | | 90 | | | | | 95 | | | |
| Tyr | His | Leu | Val | Thr | Glu | Val | Arg | Gly | Met | Gln | Glu | Ala | Pro | Glu | Ala |
| 100 | | | | | | | 105 | | | | | 110 | | | |
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| Arg | Asp | Leu | Phe | Asp | Arg | Ala | Val | Val | Leu | Ser | His | Tyr | Ile | His | Asn |
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| Leu | Ser | Ser | Glu | Met | Phe | Ser | Glu | Phe | Asp | Lys | Arg | Tyr | Thr | His | Gly |
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| Ala | Thr | Pro | Glu | Asp | Lys | Glu | Gln | Ala | Gln | Gln | Met | Asn | Gln | Lys | Asp |
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| Tyr | His | Leu | Val | Thr | Glu | Val | Arg | Gly | Met | Gln | Glu | Ala | Pro | Glu | Ala |
| 100 | | | | | | | 105 | | | | | 110 | | | |
| Ile | Leu | Ser | Lys | Ala | Val | Glu | Ile | Glu | Glu | Gln | Thr | Lys | Arg | Leu | Leu |
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35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
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Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
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Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
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Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Arg Pro Pro
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35 40 45

Ser Gln Thr Ser Phe Cys Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60

Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95

Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
100 105 110

His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Arg Arg Thr Gly Gln Ile Leu Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn His Asp Ala Leu Leu Lys Asn
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35 40 45

Ser Gln Thr Ser Phe Ser Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60

Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95

Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
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His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
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Leu Glu Asp Gly Ser Pro Arg
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<213> Homo sapiens

<400> 23
Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 24
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Ser Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro
 130

<210> 25
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 25
 atgttcccaa ccattccctt atccaggctt tttgacaacg ctatgctccg cgcccgctgc 60
 ctgtaccagc tggcatatga cacctatcg gagtttgaag aagcctatat cctgaaggag 120
 cagaagtatt cattcctgca gaaccccccag acctccctct gcttctcaga gtctattcca 180
 acacccctcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcacatctcc 240
 ctgctgctca tccagtcatg gctggagccc gtgcagctcc tcaggagcgt ctgcgccaac 300
 agcctgggtgt atggcgccctc ggacagcaac gtctatcgcc acctgaagga cctagagggaa 360
 ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
 aatcagtccct acagcaagtt tgacacaaaa tcgcacacaacg atgacgcact gctcaagaac 480
 tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcatac 540
 gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 26
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 26
 atgttcccaa ccattccctt atccaggctt tttgacaacg ctatgctccg cgcccgctgc 60
 ctgtaccagc tggcatatga cacctatcg gagtttgaag aagcctatat cctgaaggag 120
 cagaagtatt cattcctgca gaaccccccag acctccctct gcttctcaga gtctattcca 180
 acacccctcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcacatctcc 240
 ctgctgctca tccagtcatg gctggagccc gtgcagctcc tcaggagcgt ctgcgccaac 300
 agcctgggtgt atggcgccctc ggacagcaac gtctatcgcc acctgaagga cctagagggaa 360
 ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
 aatcagtccct acagcaagtt tgacacaaaa tcgcacacaacg atgacgcact gctcaagaac 480
 tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcatac 540
 gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 27

<211> 579
<212> DNA
<213> Homo sapiens

<400> 27

tacaagggtt ggtaaggaa taggtccgaa aaactgttgc gatacgaggc gcgggcagcg 60
gacatggtcg accgtatact gtggatagtc ctc当地actc ttcgatata ggacttcctc 120
gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtgaaaggt tgtcccactt ttgcgtcgta tttagattgg atctcgacga ggcgttagagg 240
gacgacgagt aggtcgtac cgc当地cggg cacgtcgagg agtccctcgca gaagcgggt 300
tcggaccaca taccgcggag cctgtcggtt cagatagcgg tggacttcctt gatctcctt 360
ccgttaggtt ggc当地acac ctccgacctt ctaccgtcg gggcctgacc cgtctagaag 420
ttagtcagga tgtcgtaa actgtgtttt agcgtgttgc tactgcgtga cgagttctt 480
atgccc当地cag agatgacgaa gtc当地tcctg tacctgttcc agctctgtaa ggacgcgt 540
cagtcacgg cgagacaccc cccgtcgaca cc当地agatc 579

<210> 28

<211> 579
<212> DNA
<213> Homo sapiens

<400> 28

tacaagggtt ggtaaggaa taggtccgaa aaactgttgc gatacgaggc gcgggcagcg 60
gacatggtcg accgtatact gtggatagtc ctc当地actc ttcgatata ggacttcctc 120
gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtgaaaggt tgtcccactt ttgcgtcgta tttagattgg atctcgacga ggcgttagagg 240
gacgacgagt aggtcgtac cgc当地cggg cacgtcgagg agtccctcgca gaagcgggt 300
tcggaccaca taccgcggag cctgtcggtt cagatagcgg tggacttcctt gatctcctt 360
ccgttaggtt ggc当地acac ctccgacctt ctaccgtcg gggcctgacc cgtctagaag 420
ttagtcagga tgtcgtaa actgtgtttt agcgtgttgc tactgcgtga cgagttctt 480
atgccc当地cag agatgacgaa gtc当地tcctg tacctgttcc agctctgtaa ggacgcgt 540
cagtcacgg cgagacaccc cccgtcgaca cc当地agatc 579

<210> 29

<211> 192
<212> PRT
<213> Homo sapiens

<400> 29

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

| | | | |
|---|-----|-----|-----|
| 65 | 70 | 75 | 80 |
| Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser | | | |
| 85 | 90 | 95 | |
| Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr | | | |
| 100 | 105 | 110 | |
| Arg His Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg | | | |
| 115 | 120 | 125 | |
| Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr | | | |
| 130 | 135 | 140 | |
| Ser Lys Phe Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn | | | |
| 145 | 150 | 155 | 160 |
| Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr | | | |
| 165 | 170 | 175 | |
| Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe | | | |
| 180 | 185 | 190 | |

<210> 30
 <211> 135
 <212> PRT
 <213> Homo sapiens

| | | | |
|---|----|----|----|
| <400> 30 | | | |
| Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu | | | |
| 1 | 5 | 10 | 15 |
| Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe | | | |
| 20 | 25 | 30 | |
| Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn | | | |
| 35 | 40 | 45 | |
| Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn | | | |
| 50 | 55 | 60 | |
| Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser | | | |
| 65 | 70 | 75 | 80 |
| Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser | | | |
| 85 | 90 | 95 | |
| Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr | | | |

100

105

110

Arg His Leu Lys Asp Leu Glú Glu Gly Ile Gln Thr Leu Met Trp Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg
130 135

<210> 31
<211> 18
<212> DNA
<213> Homo sapiens

<400> 31
cctgaaacca aagaaaaat 18

<210> 32
<211> 6
<212> PRT
<213> Homo sapiens

<400> 32
Pro Glu Thr Lys Glu Asn
1 5

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide
sequence coding for specific cleavage site of the
IgA protease

<400> 33
cctagacccc caacacct 18

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: specific
cleavage site of the IgA protease

<400> 34
Pro Arg Pro Pro Thr Pro
1 5